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Insights into the mechanism of recruitment of different membrane-binding domains of Arabidopsis thaliana using computational approaches.¹ SHANEEN SINGH, RAHIMAH AHMAD, EWA WYWIAL, Brooklyn College — Arabidopsis thaliana, commonly known as Mouse Ear Cress, serves as a model organism for understanding various signaling pathways in plants and comparing them with those of other organisms. Although plants share several similarities in signaling mechanisms and pathways with other organisms, an emerging theme is that there are also several instances of striking differences and unique mechanisms that are found only in plants. One of the most understudied signaling pathways in plants are those that involve lipids as second messengers and involve membrane recruitment of signaling proteins as an integral part of the signaling pathway. Important components in lipid signaling are lipid binding domains that recruit their parent proteins to the membrane to carry out the signaling. This study focuses on several membrane targeting domains found in Arabidopsis thaliana using computational techniques to elucidate their membrane binding function. We have identified all instances of these domains in the genome of Arabidopsis thaliana using manual and automated methods, created three dimensional models for each sequence, and analyzed their biophysical/biochemical properties. Our studies lay the foundation for understanding the role of these domains in plants, which is largely unexplored and contributes to the mechanisms of membrane binding in general.

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